```
OM of: US-09-331-631-5_COPY_1_32 to: N_Geneseq_36:*   out_format : pfs

Date: May 13, 2000 11:15 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlp
 -Q=/cgn2_1/USPTO_spool/US09331631/runat_11052000_144018_21048/app_query.fasta.1
 -DB=N_Geneseq_36 -QFMT=fastap -SUFFIX=rng -GAPOP=12.000
 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
 -MAXLEN=1000000 -USER=US09331631 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
 -THREADS=1

Search information block:
Query: US-09-331-631-5_COPY_1_32
Query length: 32
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 124.060000


score_list:
Sequence              Strd Orig    ZScore    EScore Len  ! Documentation  ..
N_Geneseq_36:V42316    +  180.00  474.48  7.9e-19   2140  ! Macadamia integrifolia partial
N_Geneseq_36:V42310    +  180.00  474.34  8.1e-19   2171  ! Macadamia integrifolia antimic
N_Geneseq_36:V42311    +  180.00  474.34  8.1e-19   2171  ! Macadamia integrifolia antimic
N_Geneseq_36:V10493    +   64.50  163.97  0.1563     656  ! Human TSP1 genomic DNA. Complex
N_Geneseq_36:V10494    +   64.50  157.26  0.3697    1326  ! Human TSP1 concatamer genomic
N_Geneseq_36:T63077    +   59.00  145.55  1.66       908  ! Active clone NZ4 of IgG-Fc bind
N_Geneseq_36:T63078    +   59.00  141.86  2.66      1336  ! Active clone C72 of IgG-Fc bin
N_Geneseq_36:T63073    +   59.00  125.00  23.14     7824  ! 7.8 kb fragment of pNV11-ST. D
N_Geneseq_36:T63074    +   59.00  117.95  57.16    16382  ! IgG-Fc binding protein coding
N_Geneseq_36:X03798    +   55.00  122.00  34.03     3334  ! Arabidopsis enhanced disease s
N_Geneseq_36:X03800    +   52.00  118.02  56.67     2106  ! Arabidopsis enhanced disease s
N_Geneseq_36:X03804    +   52.00  108.46  193.25    5740  ! Arabidopsis mutant EDS1 gene d
N_Geneseq_36:X03796    +   52.00  108.45  193.33    5742  ! Arabidopsis La-er enhanced dis
N_Geneseq_36:X03801    +   52.00  108.45  193.33    5742  ! Arabidopsis mutant EDS1 gene d
N_Geneseq_36:X03806    +   52.00  108.45  193.33    5742  ! Arabidopsis mutant EDS1 gene d
N_Geneseq_36:X03807    +   52.00  108.45  193.33    5742  ! Arabidopsis mutant EDS1 gene d
N_Geneseq_36:X03808    +   52.00  108.45  193.33    5742  ! Arabidopsis mutant EDS1 gene d
N_Geneseq_36:Q86989    +   51.00  121.04  38.48     1146  ! Creatine-kinase subunit B cDNA
N_Geneseq_36:Q51619    +   51.00  119.29  48.13     1376  ! Human creatine kinase subunit
N_Geneseq_36:N81538    +   50.50  106.30  254.66    4641  ! Sequence of a gene fragment cc
N_Geneseq_36:T15931    +   49.50   99.75  590.23    6889  ! DHFR/intron (WTrasSD)-TnFr-IgG
N_Geneseq_36:X13026    -   49.50   89.55  2.2e+03  20072  ! Enterococcus faecalis genome
N_Geneseq_36:X27434    -   49.00  116.47  69.17     1032  ! Human secreted protein gene 5
N_Geneseq_36:X27315    -   49.00  116.45  69.34     1034  ! Human secreted protein gene 5
N_Geneseq_36:X03799    +   49.00  108.91  182.33    2279  ! Arabidopsis enhanced disease s
N_Geneseq_36:V30458_4  +   49.00   71.93  2.1e+04  110000  ! Continuation (5 of 6) of V3
N_Geneseq_36:V30459_4  +   49.00   71.93  2.1e+04  110000  ! Continuation (5 of 6) of V3
N_Geneseq_36:T31487    -   48.00  116.65  67.57      756  ! Maleate isomerase coding sequen
N_Geneseq_36:V32619    +   48.00  106.83  238.02    2116  ! Mouse preprotachykinin-C (PPT-
N_Geneseq_36:T36507    -   48.00  101.83  451.82    3573  ! 3.5 kb DNA contg. ars region,
N_Geneseq_36:V46476    -   47.50  113.91  96.07      871  ! Human Kp43 cDNA. DNA encoding p
N_Geneseq_36:V72243    +   47.50  106.35  253.32    1924  ! G. max SBP2 cDNA. New modified
N_Geneseq_36:Q75303    +   47.50   98.79  667.38    4247  ! Human astrovirus serotype 2 ge
N_Geneseq_36:Q75302    +   47.50   94.26  1.2e+03   6828  ! Genomic RNA of human astroviru
N_Geneseq_36:T41849    +   47.00  101.45  474.50    2777  ! Bacillus cellulase BCE 113 gen
N_Geneseq_36:V21209_13 -   47.00   66.36  4.1e+04  110000  ! Continuation (14 of 17) of
N_Geneseq_36:X12323    +   46.50  131.48  10.08      103  ! Human biallelic polymorphic DNA
N_Geneseq_36:X40197    +   46.50  103.29  375.06     1980  ! Sequence of C3Vs gene. New isc
N_Geneseq_36:V52204    -   46.50   76.52  1.2e+04   32768  ! Streptococcus pneumoniae genc
N_Geneseq_36:Q66845    -   46.00  117.17  63.18      399  ! Sequence encoding the light cha
N_Geneseq_36:V54350    +   46.00  115.06  82.86      498  ! Human mitochondrial hinge prote
N_Geneseq_36:V99255    +   46.00  108.31  196.80    1010  ! DNA encoding an active acyl
N_Geneseq_36:T60712    +   46.00  104.02  341.29    1584  ! Saccharomyces cerevisiae te
N_Geneseq_36:V69098    +   46.00  101.64  463.43    2034  ! Mouse growth hormone recept
N_Geneseq_36:Q27387    +   46.00  100.33  548.09    2333  ! Clone pY2 encoding part of

seq_name: N_Geneseq_36:V42316

seq_documentation_block:
ID   V42316 standard; cDNA; 2140 BP.
AC   V42316;
DT   27-OCT-1998  (first entry)
DE   Macadamia integrifolia partialantimicrobial protein gene.
KW   antimicrobial protein; infestation; control; ss.
OS   Macadamia integrifolia.
FH   Key             Location/Qualifiers
FT   CDS             1. .1878
FT                   /*tag=  a
FT                   /product= partial antimicrobial protein
FT   mat_peptide     1. .1875
FT                   /*tag=  b
PN   WO9827805-A1.
PD   02-JUL-1998.
PF   22-DEC-1997; AU0874.
PR   20-DEC-1996; AU-004275.
PA   (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI   Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR   WPI; 98-377279/32.
DR   P-PSDB; W62830.
PT   Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT   useful for controlling microbial infestations of plants or mammals
PS   Claim 5; Page 46-47; 96pp; English.
CC   The sequence is that encoding an antimicrobial protein which can
CC   be used to control microbial infestations in plants and mammalian
CC   animals.
SQ   Sequence   2140 BP;    695 A;    486 C;    557 G;    402 T;


alignment_scores:
           Quality:  180.00              Length:     32
             Ratio:  5.625                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-331-631-5_COPY_1_32 x V42316   ..

 Align seg 1/1  to: V42316  from: 1  to: 2140

       1 GlnCysMetGlnLeuGluThrSerGlyGlnMetArgArgCysValSerGl 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
       1 CAATGCATGCAGTTAGAGACATCAGGCCAGATGCGTCGGTGTGTGAGTCA 50

      17 nCysAspLysArgPheGluGluAspIleAspTrpSerLysTyrAsp 32
         ||||||||||||||||||||||||||||||||||||||||||||||||
      51 GTGCGATAAGAGATTTGAAGAGGATATAGATTGGTCTAAGTATGAT 96

seq_name: N_Geneseq_36:V42310

seq_documentation_block:
ID   V42310 standard; cDNA; 2171 BP.
AC   V42310;
DT   27-OCT-1998  (first entry)
DE   Macadamia integrifolia antimicrobial protein gene.
KW   antimicrobial protein; infestation; control; ss.
OS   Macadamia integrifolia.
FH   Key             Location/Qualifiers
FT   CDS             1. .2001
FT                   /*tag=  a
FT                   /product= antimicrobial protein
FT   sig_peptide     1. .85
FT                   /*tag=  b
FT   mat_peptide     86. .1999
FT                   /*tag=  c
PN   WO9827805-A1.
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PD   02-JUL-1998.
PF   22-DEC-1997; AU0874.
PR   20-DEC-1996; AU-004275.
PA   (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI   Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR   WPI; 98-377279/32.
DR   P-PSDB; W62828.
PT   Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT   useful for controlling microbial infestations of plants or mammals
PS   Claim 5; Page 37-38; 96pp; English.
CC   The sequence is that encoding an antimicrobial protein which can
CC   be used to control microbial infestations in plants and mammalian
CC   animals.
SQ   Sequence   2171 BP;    687 A;    507 C;    570 G;    407 T;


alignment_scores:
            Quality:  180.00             Length:     32
              Ratio:  5.625                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-331-631-5_COPY_1_32 x V42310   ..

 Align seg 1/1  to: V42310  from: 1  to: 2171

       1 GlnCysMetGlnLeuGluThrSerGlyGlnMetArgArgCysValSerGl 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     124 CAATGCATGCAGTTGGAGACATCAGGCCAGATGCGTCGGTGTGTGAGTCA 173

      17 nCysAspLysArgPheGluGluAspIleAspTrpSerLysTyrAsp 32
         ||||||||||||||||||||||||||||||||||||||||||||||
     174 GTGCGATAAGAGATTTGAAGAGGATATAGATTGGTCTAAGTATGAT 219

seq_name: N_Geneseq_36:V42311

seq_documentation_block:
ID   V42311 standard; cDNA; 2171 BP.
AC   V42311;
DT   27-OCT-1998  (first entry)
DE   Macadamia integrifolia antimicrobial protein gene.
KW   antimicrobial protein; infestation; control; ss.
OS   Macadamia integrifolia.
FH   Key             Location/Qualifiers
FT   CDS             1. .2001
FT                   /*tag=  a
FT                   /product= antimicrobial protein
FT   sig_peptide     1. .86
FT                   /*tag=  b
FI   mat_peptide     87. .1999
FT                   /*tag=  c
PN   WO9827805-A1.
PD   02-JUL-1998.
PF   22-DEC-1997; AU0874.
PR   20-DEC-1996; AU-004275.
PA   (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI   Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR   WPI; 98-377279/32.
DR   P-PSDB; W62829.
PT   Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT   useful for controlling microbial infestations of plants or mammals
PS   Claim 5; Page 41-43; 96pp; English.
CC   The sequence is that encoding an antimicrobial protein which can
CC   be used to control microbial infestations in plants and mammalian
CC   animals.
SQ   Sequence   2171 BP;    680 A;    509 C;    571 G;    411 T;


alignment_scores:
            Quality:  180.00             Length:     32
              Ratio:  5.625                Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-331-631-5_COPY_1_32 x V42311   ..

 Align seg 1/1  to: V42311  from: 1  to: 2171

       1 GlnCysMetGlnLeuGluThrSerGlyGlnMetArgArgCysValSerGl 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     124 CAATGCATGCAGTTGGAGACATCAGGCCAGATGCGTCGGTGTGTGAGTCA 173

      17 nCysAspLysArgPheGluGluAspIleAspTrpSerLysTyrAsp 32
         ||||||||||||||||||||||||||||||||||||||||||||||
     174 GTGCGATAAGAGATTTGAAGAGGATATAGATTGGTCTAAGTATGAT 219

seq_name: N_Geneseq_36:V10493

seq_documentation_block:
ID   V10493 standard; DNA; 656 BP.
AC   V10493;
DT   18-AUG-1998  (first entry)
DE   Human TSP1 genomic DNA.
KW   TSP1; thrombospondin; anti-angiogenic; cationic vehicle; gene therapy;
KW   liposome; DNA complex; tumour suppressor protein; treatment; neoplastic;
KW   metabolic disease; tumour; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             1. .656
FT                   /*tag=  a
FT                   /product= TSP1
FT                   /note= "Thrombospondin I"
FT                   /transl_except= (pos: 478. .480, aa: Thr)
FT                   /transl_except= (pos: 649. .650, aa: Arg)
PN   EP-819758-A2.
PD   21-JAN-1998.
PF   16-JUL-1997; 112154.
PR   16-JUL-1996; US-680845.
PA   (MIXS/) MIXSON A J.
PI   Mixson AJ;
DR   WPI; 98-078839/08.
DR   P-PSDB; W40287.
PT   Complexes of DNA encoding anti-angiogenic peptide - with cationic
PT   liposome(s) or cationic polymer, useful for, e.g. gene therapy of
PT   tumours
PS   Claim 24; Page 6; 47pp; English.
CC   This genomic DNA sequence encodes the thrombospondin gene TSP1 which is
CC   used in a method to produce a cationic vehicle consisting of a cationic
CC   liposome:DNA complex where the DNA encodes an anti-angiogenic peptide or
CC   tumour suppressor protein. Such complexes are used for treatment of
CC   neoplastic and metabolic diseases especially for gene therapy of tumours.
SQ   Sequence   656 BP;    156 A;    174 C;    186 G;    140 T;


alignment_scores:
            Quality:   64.50             Length:     26
              Ratio:  3.395                Gaps:      1
 Percent Similarity:  73.077   Percent Identity: 46.154

alignment_block:
 US-09-331-631-5_COPY_1_32 x V10493   ..

 Align seg 1/1  to: V10493  from: 1  to: 656

       7 ThrSerGlyGlnMetArgArgCys...ValSerGlnCysAspLysArgPh 22
         :::|||   |||   |||   |||   :::::::::|||||||||||||
     346 TCCTCGGTCCAGACACGGACCTGCCACATTCAGGAGTGTGACAAAAGATT 395

      22 eGluGluAspIleAspTrpSerLysTyr 31
         |:::::|||      ||||||   :::
     396 TAAACAGGATGGTGGCTGGAGCCACTGG 423

seq_name: N_Geneseq_36:V10494

seq_documentation_block:
ID   V10494 standard; DNA; 1326 BP.
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```
AC   V10494;
DT   18-AUG-1998  (first entry)
DE   Human TSP1 concatamer genomic DNA.
KW   TSP1; thrombospondin; anti-angiogenic; cationic vehicle; gene therapy;
KW   liposome; DNA complex; tumour suppressor protein; treatment; neoplastic;
KW   metabolic disease; tumour; concatamer; ss.
OS   Homo sapiens.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   CDS             1. .1326
FT                   /*tag= a
FT                   /transl_except= (pos: 478. .480, aa: Thr)
FT                   /transl_except= (pos: 661. .663, aa: His)
FT                   /transl_except= (pos: 1147. .1149, aa: Thr)
FT   misc_feature    658. .669
FT                   /*tag= b
FT                   /note= "intervening sequence as given in the
FT                         specification"
PN   EP-819758-A2.
PD   21-JAN-1998.
PF   16-JUL-1997; 112154.
PR   16-JUL-1996; US-680845.
PA   (MIXS/) MIXSON A J.
PI   Mixson AJ;
DR   WPI; 98-078839/08.
DR   P-PSDB; W40288.
PT   Complexes of DNA encoding anti-angiogenic peptide - with cationic
PT   liposome(s) or cationic polymer, useful for, e.g. gene therapy of
PT   tumours
PS   Claim 24; Page 7; 47pp; English.
CC   This genomic DNA sequence encodes a concatamer of the thrombospondin gene
CC   TSP1 which is used in a method to produce a cationic vehicle consisting
CC   of a cationic liposome:DNA complex where the DNA encodes an
CC   anti-angiogenic peptide or tumour suppressor protein. Such complexes are
CC   used for treatment of neoplastic and metabolic diseases especially for
CC   gene therapy of tumours.
SQ   Sequence   1326 BP;    313 A;    352 C;    378 G;    283 T;


alignment_scores:
            Quality:   64.50             Length:     26
              Ratio:  3.395               Gaps:      1
 Percent Similarity:  73.077   Percent Identity: 46.154

alignment_block:
 US-09-331-631-5_COPY_1_32 x V10494   ..

 Align seg 1/1  to: V10494  from: 1  to: 1326

       7 ThrSerGlyGlnMetArgArgCys...ValSerGlnCysAspLysArgPh 22
         :::|||   |||   |||   |||   :::::::::|||||||||||||||
     346 TCCTCGGTCCAGACACGGACCTGCCACATTCAGGAGTGTGACAAAAGATT 395

      22 eGluGluAspIleAspTrpSerLysTyr 31
         |:::::::|||      ||||||   :::
     396 TAAACAGGATGGTGGCTGGAGCCACTGG 423

seq_name: N_Geneseq_36:T63077

seq_documentation_block:
ID   T63077 standard; cDNA; 908 BP.
AC   T63077;
DT   13-MAY-1997  (first entry)
DE   Active clone NZ4 of IgG-Fc binding protein.
KW   Fragment 13; pNV11-ST; IgG-Fc binding protein; immunoglobulin; K17;
KW   human; colonic epithelium; monoclonal antibody; K9; probe; primer; ds.
OS   Homo sapiens.
PN   WO9527057-A1.
PD   12-OCT-1995.
PF   03-APR-1995; J00638.
PR   01-APR-1994; JP-129487.
PR   24-AUG-1994; JP-222547.
PR   30-MAR-1995; JP-109927.
PA   (CHUS ) CHUGAI SEIYAKU KK.
PI   Harada N,  Morikawa M;
DR   WPI; 95-358632/46.
PT   DNA derived from colonic epithelium encoding IgG-Fc binding protein
PT   - used in the mapping and analysis of IgG-Fc binding protein mRNA
PS   Example 8; Page 60; 132pp; Japanese.
CC   The sequences given in T63077-81 represent active clones of the IgG-Fc
CC   binding protein of human colonic epithelium.  mRNA isolated from human
CC   colonic epithelial tissue was used to prepare a cDNA library.  This
CC   library was screened using monoclonal antibodies K9 and K17 which bind
CC   to the large and small components of the binding protein.  These active
CC   clones were used to derive probes for screening a second DNA library
CC   from human colonic epithelial tissue.
SQ   Sequence   908 BP;    194 A;    274 C;    254 G;    186 T;


alignment_scores:
            Quality:   59.00             Length:     28
              Ratio:  2.950               Gaps:      0
 Percent Similarity:  71.429   Percent Identity: 35.714

alignment_block:
 US-09-331-631-5_COPY_1_32 x T63077   ..

 Align seg 1/1  to: T63077  from: 1  to: 908

       1 GlnCysMetGlnLeuGluThrSerGlyGlnMetArgArgCysValSerGl 17
         :::|||:::   :::      :::|||:::   |||||||||:::::||
     470 GAATGTCAAGGAGTTTGCCGTGGTGGCCGGTGCCGCAGGTGCCTCGGTCA 519

      17 nCysAspLysArgPheGluGluAspIleAspTrp 28
         ||||      :::      :::|||||||:::|||
     520 GTGTCACGCTGAAGGGGTCAGTGACATTCAATGG 553

seq_name: N_Geneseq_36:T63078

seq_documentation_block:
ID   T63078 standard; cDNA; 1336 BP.
AC   T63078;
DT   13-MAY-1997  (first entry)
DE   Active clone C72 of IgG-Fc binding protein.
KW   Fragment 13; pNV11-ST; IgG-Fc binding protein; immunoglobulin; K17;
KW   human; colonic epithelium; monoclonal antibody; K9; probe; primer; ds.
OS   Homo sapiens.
PN   WO9527057-A1.
PD   12-OCT-1995.
PF   03-APR-1995; J00638.
PR   01-APR-1994; JP-129487.
PR   24-AUG-1994; JP-222547.
PR   30-MAR-1995; JP-109927.
PA   (CHUS ) CHUGAI SEIYAKU KK.
PI   Harada N,  Morikawa M;
DR   WPI; 95-358632/46.
PT   DNA derived from colonic epithelium encoding IgG-Fc binding protein
PT   - used in the mapping and analysis of IgG-Fc binding protein mRNA
PS   Example 8; Page 61; 132pp; Japanese.
CC   The sequences given in T63077-81 represent active clones of the IgG-Fc
CC   binding protein of human colonic epithelium.  mRNA isolated from human
CC   colonic epithelial tissue was used to prepare a cDNA library.  This
CC   library was screened using monoclonal antibodies K9 and K17 which bind
CC   to the large and small components of the binding protein.  These active
CC   clones were used to derive probes for screening a second DNA library
CC   from human colonic epithelial tissue.
SQ   Sequence   1336 BP;    270 A;    404 C;    397 G;    265 T;


alignment_scores:
            Quality:   59.00             Length:     28
              Ratio:  2.950               Gaps:      0
 Percent Similarity:  71.429   Percent Identity: 35.714

alignment_block:
 US-09-331-631-5_COPY_1_32 x T63078   ..
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 Align seg 1/1  to: T63078  from: 1  to: 1336

       1 GlnCysMetGlnLeuGluThrSerGlyGlnMetArgArgCysValSerGl 17
         :::|||:::   :::      :::|||:::   |||||||||:::::::||
     325 GAATGTCAAGGAGTTTGCCGTGGTGGCCGGTGCCGCAGGTGCCTCGGTCA 374

      17 nCysAspLysArgPheGluGluAspIleAspTrp 28
         ||||      :::      :::|||||:::|||
     375 GTGTCACGCTGAAGGGGTCAGTGACATTCAATGG 408

seq_name: N_Geneseq_36:T63073

seq_documentation_block:
ID   T63073 standard; cDNA; 7824 BP.
AC   T63073;
DT   13-MAY-1997  (first entry)
DE   7.8 kb fragment of pNV11-ST.
KW   Fragment 13; pNV11-ST; IgG-Fc binding protein; immunoglobulin; K17;
KW   human; colonic epithelium; monoclonal antibody; K9; probe; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             21. .7802
FT                   /*tag=  a
FT                   /note= "CDS does not contain a stop codon"
PN   WO9527057-A1.
PD   12-OCT-1995.
PF   03-APR-1995; J00638.
PR   01-APR-1994; JP-129487.
PR   24-AUG-1994; JP-222547.
PR   30-MAR-1995; JP-109927.
PA   (CHUS ) CHUGAI SEIYAKU KK.
PI   Harada N,  Morikawa M;
DR   WPI; 95-358632/46.
DR   P-PSDB; W14748.
PT   DNA derived from colonic epithelium encoding IgG-Fc binding protein
PT   - used in the mapping and analysis of IgG-Fc binding protein mRNA
PS   Claim 1; Page 71-84; 132pp; Japanese.
CC   This sequence represents fragment 13 which is a NotI/KpnI fragment
CC   from pNV11-ST.  This sequence encodes a portion of the IgG-Fc binding
CC   protein of human colonic epithelium.  This sequence was used in the
CC   isolation of the full length sequence given in T63074.  mRNA isolated
CC   from human colonic epithelial tissue was used to prepare a cDNA library.
CC   This was screened using monoclonal antibodies K9 and K17 which bind to
CC   the large and small components of the binding protein.  Active clones,
CC   see also T63077-81, were used to derive probes for screening a second
CC   DNA library from human colonic epithelial tissue.
SQ   Sequence   7824 BP;    1344 A;    2469 C;    2501 G;    1510 T;


alignment_scores:
           Quality:   59.00            Length:     28
             Ratio:  2.950              Gaps:      0
 Percent Similarity:  71.429   Percent Identity: 35.714

alignment_block:
 US-09-331-631-5_COPY_1_32 x T63073   ..

 Align seg 1/1  to: T63073  from: 1  to: 7824

       1 GlnCysMetGlnLeuGluThrSerGlyGlnMetArgArgCysValSerGl 17
         :::|||:::   :::      :::|||:::   |||||||||:::::::||
     482 GAATGTCAAGGAGTTTGCCGTGGTGGCCGGTGCCGCAGGTGCCTCGGTCA 531

      17 nCysAspLysArgPheGluGluAspIleAspTrp 28
         ||||      :::      :::|||||:::|||
     532 GTGTCACGCTGAAGGGGTCAGTGACATTCAATGG 565

seq_name: N_Geneseq_36:T63074

seq_documentation_block:
ID   T63074 standard; cDNA; 16382 BP.
AC   T63074;
DT   13-MAY-1997  (first entry)
DE   IgG-Fc binding protein coding sequence.
KW   Fragment 13; pNV11-ST; IgG-Fc binding protein; immunoglobulin; K17;
KW   human; colonic epithelium; monoclonal antibody; K9; probe; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   cds             9. .1626
FT                   /*tag=  a
PN   WO9527057-A1.
PD   12-OCT-1995.
PF   03-APR-1995; J00638.
PR   01-APR-1994; JP-129487.
PR   24-AUG-1994; JP-222547.
PR   30-MAR-1995; JP-109927.
PA   (CHUS ) CHUGAI SEIYAKU KK.
PI   Harada N,  Morikawa M;
DR   WPI; 95-358632/46.
DR   P-PSDB; W14749.
PT   DNA derived from colonic epithelium encoding IgG-Fc binding protein
PT   - used in the mapping and analysis of IgG-Fc binding protein mRNA
PS   Claim 3; Page 86-113; 132pp; Japanese.
CC   This sequence encodes the IgG-Fc binding protein of human colonic
CC   epithelium.  This sequence was isolated using the sequence given in
CC   T63073.  mRNA isolated from human colonic epithelial tissue was used
CC   to prepare a cDNA library.  This was screened using monoclonal antibodies
CC   K9 and K17 which bind to the large and small components of the binding
CC   protein.  Active clones, see also T63077-81, were used to derive probes
CC   for screening a second DNA library from human colonic epithelial tissue.
SQ   Sequence   16382 BP;    2803 A;    5193 C;    5206 G;    3180 T;


alignment_scores:
           Quality:   59.00            Length:     28
             Ratio:  2.950              Gaps:      0
 Percent Similarity:  71.429   Percent Identity: 35.714

alignment_block:
 US-09-331-631-5_COPY_1_32 x T63074   ..

 Align seg 1/1  to: T63074  from: 1  to: 16382

       1 GlnCysMetGlnLeuGluThrSerGlyGlnMetArgArgCysValSerGl 17
         :::|||:::   :::      :::|||:::   |||||||||:::::::||
     470 GAATGTCAAGGAGTTTGCCGTGGTGGCCGGTGCCGCAGGTGCCTCGGTCA 519

      17 nCysAspLysArgPheGluGluAspIleAspTrp 28
         ||||      :::      :::|||||:::|||
     520 GTGTCACGCTGAAGGGGTCAGTGACATTCAATGG 553

seq_name: N_Geneseq_36:X03798

seq_documentation_block:
ID   X03798 standard; DNA; 3334 BP.
AC   X03798;
DT   01-APR-1999  (first entry)
DE   Arabidopsis enhanced disease susceptibility gene Eds1col.
KW   Arabidopsis; Lansdberg-erecta; La-er; Wassilewskija; Ws-0; EDS1;
KW   enhanced disease susceptibility; Columbia; Col-0; Eds1ler; Eds1col;
KW   Eds1ws; disease resistance; esterase; lipase; ss.
OS   Arabidopsis sp.
FH   Key             Location/Qualifiers
FT   CDS             1054. .3193
FT                   /*tag=  a
FT                   /note= "contains introns"
FT   exon            1054. .1371
FT                   /*tag=  b
FT                   /number= 1
FT   intron          1372. .1447
FT                   /*tag=  c
FT                   /number= 1
FT   exon            1448. .2179
FT                   /*tag=  d
FT                   /number= 2
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FT   intron          2180. .2275
FT                   /*tag= e
FT                   /number= 2
FT   exon            2276. .2356
FT                   /*tag= f
FT                   /number= 3
FT   intron          2357. .2452
FT                   /*tag= g
FT                   /number= 3
FT   exon            2453. .3193
FT                   /*tag= h
FT                   /number= 4
PN   WO9853073-A1.
PD   26-NOV-1998.
PF   15-MAY-1998; G01406.
PR   16-MAY-1997; GB-010044.
PA   (PLAN-) PLANT BIOSCIENCE LTD.
PI   Falk AB, Feys BJF, Parker JE;
DR   WPI; 99-059744/05.
DR   P-PSDB; W30622.
PT   Arabidopsis gene, EDS1, modulating pathogen resistance response -
PT   useful, e.g. to produce transgenic plants, especially crops, with
PT   reduced or enhanced pathogen resistance and to isolate homologous
PT   genes
PS   Claim 3; Fig 5; 90pp; English.
CC   The present sequence encodes an enhanced disease susceptibility gene
CC   (EDS1), designated Eds1col, from Arabidopsis. EDS1 nucleic acid
CC   sequences can be used to produce transgenic plants (especially crop
CC   plants) containing transformed cells which incorporate sequences
CC   encoding EDS1 polypeptides/variant polypeptides. By allowing expression
CC   of these sequences, plant defence responses can be modulated (either
CC   enhanced or inhibited); in particular, pathogen resistance can be raised
CC   (especially if a pathogen-inducible promoter is used and/or pathogen
CC   resistance is mediated by an R gene (i.e. a plant gene) of the
CC   TIR-NBS-LRR type). EDS1 nucleic acid sequences can be used to produce
CC   probes/primers useful to identify the EDS1 sequences/similar genes, and
CC   especially to clone EDS1 homologues e.g. from other crop species, or to
CC   monitor segregation of a resistance gene. The polynucleotides or
CC   complementary sequences can also be used to downwardly modulate EDS1
CC   expression in plants, e.g. by using known antisense or co-suppression
CC   techniques or ribozymes. The polypeptides may be useful as esterases,
CC   particularly as lipases in lipid-based signalling pathways. They may
CC   also be used to produce antibodies, useful to identify/isolate the
CC   polypeptides.
SQ   Sequence   3334 BP;    1076 A;    601 C;    705 G;    952 T;


alignment_scores:
            Quality:   55.00            Length:     25
              Ratio:  3.438              Gaps:      1
 Percent Similarity:  64.000   Percent Identity: 48.000

alignment_block:
 US-09-331-631-5_COPY_1_32 x X03798   ..

 Align seg 1/1  to: X03798  from: 1  to: 3334

       6 GluThrSerGlyGlnMetArgArgCysValSerGlnCysAspLysArgPh 22
         |||:::   |||   |||::::::|||      |||         :::||
    2621 GAGGTGCTTGGTTTAATGAAGAAATGT......CAACTTCCAGATGAGTT 2664

      22 eGluGluAspIleAspTrpSerLys 30
         ||||   ||||||||||||   |||
    2665 CGAAGGGGACATAGATTGGATCAAG 2689

seq_name: N_Geneseq_36:X03800

seq_documentation_block:
ID   X03800 standard; cDNA; 2106 BP.
AC   X03800;
DT   01-APR-1999  (first entry)
DE   Arabidopsis enhanced disease susceptibility Eds1ler encoding cDNA.
KW   Arabidopsis; Lansdberg-erecta; La-er; Wassilewskija; Ws-0; EDS1;
KW   enhanced disease susceptibility; Columbia; Col-0; Eds1ler; Eds1col;
KW   Eds1ws; disease resistance; esterase; lipase; ss.
OS   Arabidopsis sp.
PN   WO9853073-A1.
PD   26-NOV-1998.
PF   15-MAY-1998; G01406.
PR   16-MAY-1997; GB-010044.
PA   (PLAN-) PLANT BIOSCIENCE LTD.
PI   Falk AB, Feys BJF, Parker JE;
DR   WPI; 99-059744/05.
PT   Arabidopsis gene, EDS1, modulating pathogen resistance response -
PT   useful, e.g. to produce transgenic plants, especially crops, with
PT   reduced or enhanced pathogen resistance and to isolate homologous
PT   genes
PS   Claim 3; Fig 7; 90pp; English.
CC   The present sequence encodes an enhanced disease susceptibility gene
CC   (EDS1), designated Eds1ler, from Arabidopsis. EDS1 nucleic acid
CC   sequences can be used to produce transgenic plants (especially crop
CC   plants) containing transformed cells which incorporate sequences
CC   encoding EDS1 polypeptides/variant polypeptides. By allowing expression
CC   of these sequences, plant defence responses can be modulated (either
CC   enhanced or inhibited); in particular, pathogen resistance can be raised
CC   (especially if a pathogen-inducible promoter is used and/or pathogen
CC   resistance is mediated by an R gene (i.e. a plant gene) of the
CC   TIR-NBS-LRR type). EDS1 nucleic acid sequences can be used to produce
CC   probes/primers useful to identify the EDS1 sequences/similar genes, and
CC   especially to clone EDS1 homologues e.g. from other crop species, or to
CC   monitor segregation of a resistance gene. The polynucleotides or
CC   complementary sequences can also be used to downwardly modulate EDS1
CC   expression in plants, e.g. by using known antisense or co-suppression
CC   techniques or ribozymes. The polypeptides may be useful as esterases,
CC   particularly as lipases in lipid-based signalling pathways. They may
CC   also be used to produce antibodies, useful to identify/isolate the
CC   polypeptides.
SQ   Sequence   2106 BP;    680 A;    375 C;    490 G;    561 T;


alignment_scores:
            Quality:   52.00            Length:     25
              Ratio:  3.250              Gaps:      1
 Percent Similarity:  64.000   Percent Identity: 44.000

alignment_block:
 US-09-331-631-5_COPY_1_32 x X03800   ..

 Align seg 1/1  to: X03800  from: 1  to: 2106

       6 GluThrSerGlyGlnMetArgArgCysValSerGlnCysAspLysArgPh 22
         |||:::   |||   ::::::::::|||      |||         :::||
    1337 GAGGTGCTCGGTTTATTGAAGAAATGT......CAACTTCCAGATGAGTT 1380

      22 eGluGluAspIleAspTrpSerLys 30
         ||||   ||||||||||||   |||
    1381 CGAAGGGGACATAGATTGGATCAAG 1405

seq_name: N_Geneseq_36:X03804

seq_documentation_block:
ID   X03804 standard; DNA; 5740 BP.
AC   X03804;
DT   01-APR-1999  (first entry)
DE   Arabidopsis mutant EDS1 gene designated La-er eds1-4.
KW   Arabidopsis; Lansdberg-erecta; La-er; Wassilewskija; Ws-0; EDS1;
KW   enhanced disease susceptibility; Columbia; Col-0; Eds1ler; Eds1col;
KW   Eds1ws; disease resistance; esterase; lipase; ss.
OS   Arabidopsis sp.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   CDS             1427. .2279
FT                   /*tag= a
FT                   /note= "contains introns"
FT   exon            1427. .1744
FT                   /*tag= b
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FT                   /number= 1
FT   intron          1745. .1820
FT                   /*tag=  c
FT                   /number= 1
FT   exon            1821. .2279
FT                   /*tag=  d
FT                   /number= 2
FT   misc_difference 2252
FT                   /*tag=  e
FT                   /note= "site of a deletion from 2252 to 2253 in the
FT                          wild-type (X03796)"
PN   WO9853073-A1.
PD   26-NOV-1998.
PF   15-MAY-1998; G01406.
PR   16-MAY-1997; GB-010044.
PA   (PLAN-) PLANT BIOSCIENCE LTD.
PI   Falk AB, Feys BJF, Parker JE;
DR   WPI; 99-059744/05.
DR   P-PSDB; W30626.
PT   Arabidopsis gene, EDS1, modulating pathogen resistance response -
PT   useful, e.g. to produce transgenic plants, especially crops, with
PT   reduced or enhanced pathogen resistance and to isolate homologous
PT   genes
PS   Claim 7; Fig -; 90pp; English.
CC   The present sequence encodes a mutant enhanced disease susceptibility
CC   protein (EDS1), designated La-er eds1-4, from Arabidopsis. EDS1 nucleic
CC   acid sequences can be used to produce transgenic plants (especially crop
CC   plants) containing transformed cells which incorporate sequences
CC   encoding EDS1 polypeptides/variant polypeptides. By allowing expression
CC   of these sequences, plant defence responses can be modulated (either
CC   enhanced or inhibited); in particular, pathogen resistance can be raised
CC   (especially if a pathogen-inducible promoter is used and/or pathogen
CC   resistance is mediated by an R gene (i.e. a plant gene) of the
CC   TIR-NBS-LRR type). EDS1 nucleic acid sequences can be used to produce
CC   probes/primers useful to identify the EDS1 sequences/similar genes, and
CC   especially to clone EDS1 homologues e.g. from other crop species, or to
CC   monitor segregation of a resistance gene. The polynucleotides or
CC   complementary sequences can also be used to downwardly modulate EDS1
CC   expression in plants, e.g. by using known antisense or co-suppression
CC   techniques or ribozymes. The polypeptides may be useful as esterases,
CC   particularly as lipases in lipid-based signalling pathways. They may
CC   also be used to produce antibodies, useful to identify/isolate the
CC   polypeptides.
CC   N.B. The present sequence is not given in the present specification
CC   but is derived from the sequence in X03796 as specified.
SQ   Sequence   5740 BP;    1821 A;    1048 C;    1215 G;    1656 T;


alignment_scores:
            Quality:   52.00              Length:     25
              Ratio:  3.250                Gaps:      1
 Percent Similarity:  64.000   Percent Identity: 44.000

alignment_block:
 US-09-331-631-5_COPY_1_32 x X03804   ..

 Align seg 1/1  to: X03804  from: 1  to: 5740

       6 GluThrSerGlyGlnMetArgArgCysValSerGlnCysAspLysArgPh 22
         |||:::   |||   ::::::::::|||      |||         :::||
    3016 GAGGTGCTCGGTTTATTGAAGAAATGT......CAACTTCCAGATGAGTT 3059

      22 eGluGluAspIleAspTrpSerLys 30
         ||||   ||||||||||||   |||
    3060 CGAAGGGGACATAGATTGGATCAAG 3084

seq_name: N_Geneseq_36:X03796

seq_documentation_block:
ID   X03796 standard; DNA; 5742 BP.
AC   X03796;
DT   01-APR-1999  (first entry)
DE   Arabidopsis La-er enhanced disease susceptibility gene EDS1.
KW   Arabidopsis; Lansdberg-erecta; La-er; Wassilewskija; Ws-0; EDS1;
KW   enhanced disease susceptibility; Columbia; Col-0; Eds1ler; Eds1col;
KW   Eds1ws; disease resistance; esterase; lipase; ss.
OS   Arabidopsis sp.
FH   Key             Location/Qualifiers
FT   CDS             1427. .3590
FT                   /*tag=  a
FT                   /note= "contains introns"
FT   exon            1427. .1744
FT                   /*tag=  b
FT                   /number= 1
FT   intron          1745. .1820
FT                   /*tag=  c
FT                   /number= 1
FT   exon            1821. .2552
FT                   /*tag=  d
FT                   /number= 2
FT   intron          2553. .2672
FT                   /*tag=  e
FT                   /number= 2
FT   exon            2673. .2753
FT                   /*tag=  f
FT                   /number= 3
FT   intron          2754. .2849
FT                   /*tag=  g
FT                   /number= 3
FT   exon            2850. .3590
FT                   /*tag=  h
FT                   /number= 4
PN   WO9853073-A1.
PD   26-NOV-1998.
PF   15-MAY-1998; G01406.
PR   16-MAY-1997; GB-010044.
PA   (PLAN-) PLANT BIOSCIENCE LTD.
PI   Falk AB, Feys BJF, Parker JE;
DR   WPI; 99-059744/05.
DR   P-PSDB; W30620.
PT   Arabidopsis gene, EDS1, modulating pathogen resistance response -
PT   useful, e.g. to produce transgenic plants, especially crops, with
PT   reduced or enhanced pathogen resistance and to isolate homologous
PT   genes
PS   Claim 3; Fig 3; 90pp; English.
CC   The present sequence encodes an enhanced disease susceptibility gene
CC   (EDS1), designated Eds1ler, from Arabidopsis. EDS1 nucleic acid
CC   sequences can be used to produce transgenic plants (especially crop
CC   plants) containing transformed cells which incorporate sequences
CC   encoding EDS1 polypeptides/variant polypeptides. By allowing expression
CC   of these sequences, plant defence responses can be modulated (either
CC   enhanced or inhibited); in particular, pathogen resistance can be raised
CC   (especially if a pathogen-inducible promoter is used and/or pathogen
CC   resistance is mediated by an R gene (i.e. a plant gene) of the
CC   TIR-NBS-LRR type). EDS1 nucleic acid sequences can be used to produce
CC   probes/primers useful to identify the EDS1 sequences/similar genes, and
CC   especially to clone EDS1 homologues e.g. from other crop species, or to
CC   monitor segregation of a resistance gene. The polynucleotides or
CC   complementary sequences can also be used to downwardly modulate EDS1
CC   expression in plants, e.g. by using known antisense or co-suppression
CC   techniques or ribozymes. The polypeptides may be useful as esterases,
CC   particularly as lipases in lipid-based signalling pathways. They may
CC   also be used to produce antibodies, useful to identify/isolate the
CC   polypeptides.
SQ   Sequence   5742 BP;    1821 A;    1049 C;    1216 G;    1656 T;


alignment_scores:
            Quality:   52.00              Length:     25
              Ratio:  3.250                Gaps:      1
 Percent Similarity:  64.000   Percent Identity: 44.000

alignment_block:
 US-09-331-631-5_COPY_1_32 x X03796   ..

 Align seg 1/1  to: X03796  from: 1  to: 5742
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       6 GluThrSerGlyGlnMetArgArgCysValSerGlnCysAspLysArgPh 22
         |||:::   |||   ::::::::::|||      |||         :::||
    3018 GAGGTGCTCGGTTTATTGAAGAAATGT......CAACTTCCAGATGAGTT 3061

      22 eGluGluAspIleAspTrpSerLys 30
         ||||   ||||||||||||   |||
    3062 CGAAGGGGACATAGATTGGATCAAG 3086

seq_name: N_Geneseq_36:X03801

seq_documentation_block:
ID   X03801 standard; DNA; 5742 BP.
AC   X03801;
DT   01-APR-1999  (first entry)
DE   Arabidopsis mutant EDS1 gene designated Ws eds1-1.
KW   Arabidopsis; Lansdberg-erecta; La-er; Wassilewskija; Ws-0; EDS1;
KW   enhanced disease susceptibility; Columbia; Col-0; Eds1ler; Eds1col;
KW   Eds1ws; disease resistance; esterase; lipase; ss.
OS   Arabidopsis sp.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   CDS             1427. .3590
FT                   /*tag= a
FT                   /note= "contains introns"
FT   exon            1427. .1744
FT                   /*tag= b
FT                   /number= 1
FT   intron          1745. .1820
FT                   /*tag= c
FT                   /number= 1
FT   exon            1821. .2552
FT                   /*tag= d
FT                   /number= 2
FT   intron          2553. .2672
FT                   /*tag= e
FT                   /number= 2
FT   exon            2673. .2753
FT                   /*tag= f
FT                   /number= 3
FT   intron          2754. .2849
FT                   /*tag= g
FT                   /number= 3
FT   exon            2850. .3590
FT                   /*tag= h
FT                   /number= 4
FT   misc_difference 3114
FT                   /*tag= i
FT                   /note= "wild-type G is changed to A, causing the amino
FT                          acid residue at position 466 to change from Glu
FT                          to Lys"
PN   WO9853073-A1.
PD   26-NOV-1998.
PF   15-MAY-1998; G01406.
PR   16-MAY-1997; GB-010044.
PA   (PLAN-) PLANT BIOSCIENCE LTD.
PI   Falk AB, Feys BJF, Parker JE;
DR   WPI; 99-059744/05.
DR   P-PSDB; W30624.
PT   Arabidopsis gene, EDS1, modulating pathogen resistance response -
PT   useful, e.g. to produce transgenic plants, especially crops, with
PT   reduced or enhanced pathogen resistance and to isolate homologous
PT   genes
PS   Claim 7; Fig -; 90pp; English.
CC   The present sequence encodes a mutant enhanced disease susceptibility
CC   protein (EDS1), designated Ws eds1-1, from Arabidopsis. EDS1 nucleic
CC   acid sequences can be used to produce transgenic plants (especially crop
CC   plants) containing transformed cells which incorporate sequences
CC   encoding EDS1 polypeptides/variant polypeptides. By allowing expression
CC   of these sequences, plant defence responses can be modulated (either
CC   enhanced or inhibited); in particular, pathogen resistance can be raised
CC   (especially if a pathogen-inducible promoter is used and/or pathogen
CC   resistance is mediated by an R gene (i.e. a plant gene) of the
CC   TIR-NBS-LRR type). EDS1 nucleic acid sequences can be used to produce
CC   probes/primers useful to identify the EDS1 sequences/similar genes, and
CC   especially to clone EDS1 homologues e.g. from other crop species, or to
CC   monitor segregation of a resistance gene. The polynucleotides or
CC   complementary sequences can also be used to downwardly modulate EDS1
CC   expression in plants, e.g. by using known antisense or co-suppression
CC   techniques or ribozymes. The polypeptides may be useful as esterases,
CC   particularly as lipases in lipid-based signalling pathways. They may
CC   also be used to produce antibodies, useful to identify/isolate the
CC   polypeptides.
CC   N.B. The present sequence is not given in the present specification
CC   but is derived from the sequence in X03796 as specified.
SQ   Sequence   5742 BP;    1822 A;    1049 C;    1215 G;    1656 T;


alignment_scores:
           Quality:   52.00              Length:     25
             Ratio:  3.250                Gaps:      1
 Percent Similarity:  64.000   Percent Identity: 44.000

alignment_block:
 US-09-331-631-5_COPY_1_32 x X03801   ..

 Align seg 1/1  to: X03801  from: 1  to: 5742

       6 GluThrSerGlyGlnMetArgArgCysValSerGlnCysAspLysArgPh 22
         |||:::   |||   ::::::::::|||      |||         :::||
    3018 GAGGTGCTCGGTTTATTGAAGAAATGT......CAACTTCCAGATGAGTT 3061

      22 eGluGluAspIleAspTrpSerLys 30
         ||||   ||||||||||||   |||
    3062 CGAAGGGGACATAGATTGGATCAAG 3086

seq_name: N_Geneseq_36:X03806

seq_documentation_block:
ID   X03806 standard; DNA; 5742 BP.
AC   X03806;
DT   01-APR-1999  (first entry)
DE   Arabidopsis mutant EDS1 gene designated Ws eds1-6.
KW   Arabidopsis; Lansdberg-erecta; La-er; Wassilewskija; Ws-0; EDS1;
KW   enhanced disease susceptibility; Columbia; Col-0; Eds1ler; Eds1col;
KW   Eds1ws; disease resistance; esterase; lipase; ss.
OS   Arabidopsis sp.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   CDS             1427. .2171
FT                   /*tag= a
FT                   /note= "contains introns"
FT   exon            1427. .1744
FT                   /*tag= b
FT                   /number= 1
FT   intron          1745. .1820
FT                   /*tag= c
FT                   /number= 1
FT   exon            1821. .2171
FT                   /*tag= d
FT                   /number= 2
FT   misc_difference 2169
FT                   /*tag= e
FT                   /note= "wild-type C is changed to T, causing the amino
FT                          acid residue at position 223 to change from Gln
FT                          to a stop codon"
PN   WO9853073-A1.
PD   26-NOV-1998.
PF   15-MAY-1998; G01406.
PR   16-MAY-1997; GB-010044.
PA   (PLAN-) PLANT BIOSCIENCE LTD.
PI   Falk AB, Feys BJF, Parker JE;
DR   WPI; 99-059744/05.
DR   P-PSDB; W30627.
PT   Arabidopsis gene, EDS1, modulating pathogen resistance response -
PT   useful, e.g. to produce transgenic plants, especially crops, with
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```
PT   reduced or enhanced pathogen resistance and to isolate homologous
PT   genes
PS   Claim 7; Fig -; 90pp; English.
CC   The present sequence encodes a mutant enhanced disease susceptibility
CC   protein (EDS1), designated Ws eds1-6, from Arabidopsis. EDS1 nucleic
CC   acid sequences can be used to produce transgenic plants (especially crop
CC   plants) containing transformed cells which incorporate sequences
CC   encoding EDS1 polypeptides/variant polypeptides. By allowing expression
CC   of these sequences, plant defence responses can be modulated (either
CC   enhanced or inhibited); in particular, pathogen resistance can be raised
CC   (especially if a pathogen-inducible promoter is used and/or pathogen
CC   resistance is mediated by an R gene (i.e. a plant gene) of the
CC   TIR-NBS-LRR type). EDS1 nucleic acid sequences can be used to produce
CC   probes/primers useful to identify the EDS1 sequences/similar genes, and
CC   especially to clone EDS1 homologues e.g. from other crop species, or to
CC   monitor segregation of a resistance gene. The polynucleotides or
CC   complementary sequences can also be used to downwardly modulate EDS1
CC   expression in plants, e.g. by using known antisense or co-suppression
CC   techniques or ribozymes. The polypeptides may be useful as esterases,
CC   particularly as lipases in lipid-based signalling pathways. They may
CC   also be used to produce antibodies, useful to identify/isolate the
CC   polypeptides.
CC   N.B. The present sequence is not given in the present specification
CC   but is derived from the sequence in X03796 as specified.
SQ   Sequence   5742 BP;    1821 A;    1048 C;    1216 G;    1657 T;


alignment_scores:
            Quality:   52.00              Length:     25
              Ratio:  3.250                Gaps:      1
 Percent Similarity:  64.000   Percent Identity: 44.000

alignment_block:
 US-09-331-631-5_COPY_1_32 x X03806   ..

 Align seg 1/1  to: X03806  from: 1  to: 5742

       6 GluThrSerGlyGlnMetArgArgCysValSerGlnCysAspLysArgPh 22
         |||:::   |||   :::::::::|||      |||         :::||
    3018 GAGGTGCTCGGTTTATTGAAGAAATGT......CAACTTCCAGATGAGTT 3061

      22 eGluGluAspIleAspTrpSerLys 30
         ||||   ||||||||||||   |||
    3062 CGAAGGGGACATAGATTGGATCAAG 3086
```